

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/591490
Source: 1FwP
Date Processed by STIC: 9/18/06

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IFWP

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/591,490

DATE: 09/18/2006

TIME: 15:26:44

Input Set : A:\SHIMIZU-13116_sq.txt
 Output Set: N:\CRF4\09182006\J591490.raw

3 <110> APPLICANT: KADOWAKI, Takashi
 4 YAMAUCHI, Toshimasa
 6 <120> TITLE OF INVENTION: REGULATOR FOR ADIPONECTIN RECEPTOR EXPRESSION
 8 <130> FILE REFERENCE: SHIMIZU-13116
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/591,490
 C--> 10 <141> CURRENT FILING DATE: 2006-09-01
 10 <150> PRIOR APPLICATION NUMBER: PCT/JP2005/003744
 11 <151> PRIOR FILING DATE: 2005-03-04
 13 <150> PRIOR APPLICATION NUMBER: US 60/549,561
 14 <151> PRIOR FILING DATE: 2004-03-04
 16 <160> NUMBER OF SEQ ID NOS: 15
 18 <170> SOFTWARE: PatentIn version 3.3
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 652
 22 <212> TYPE: PRT
 23 <213> ORGANISM: Mus musculus
 25 <400> SEQUENCE: 1
 27 Met Ala Glu Ala Pro Gln Val Val Glu Thr Asp Pro Asp Phe Glu Pro
 28 1 5 10 15
 31 Leu Pro Arg Gln Arg Ser Cys Thr Trp Pro Leu Pro Arg Pro Glu Phe
 32 20 25 30
 35 Asn Gln Ser Asn Ser Thr Thr Ser Ser Pro Ala Pro Ser Gly Gly Ala
 36 35 40 45
 39 Ala Ala Asn Pro Asp Ala Ala Ser Leu Ala Ser Ala Ser Ala Val
 40 50 55 60
 43 Ser Thr Asp Phe Met Ser Asn Leu Ser Leu Leu Glu Glu Ser Glu Asp
 44 65 70 75 80
 47 Phe Ala Arg Ala Pro Gly Cys Val Ala Val Ala Ala Ala Ala Ala
 48 85 90 95
 51 Ser Arg Gly Leu Cys Gly Asp Phe Gln Gly Pro Glu Ala Gly Cys Val
 52 100 105 110
 55 His Pro Ala Pro Pro Gln Pro Pro Pro Thr Gly Pro Leu Ser Gln Pro
 56 115 120 125
 59 Pro Pro Val Pro Pro Ser Ala Ala Ala Ala Gly Pro Leu Ala Gly
 60 130 135 140
 63 Gln Pro Arg Lys Thr Ser Ser Arg Arg Asn Ala Trp Gly Asn Leu
 64 145 150 155 160
 67 Ser Tyr Ala Asp Leu Ile Thr Lys Ala Ile Glu Ser Ser Ala Glu Lys
 68 165 170 175
 71 Arg Leu Thr Leu Ser Gln Ile Tyr Glu Trp Met Val Lys Ser Val Pro
 72 180 185 190
 75 Tyr Phe Lys Asp Lys Gly Asp Ser Asn Ser Ser Ala Gly Trp Lys Asn
 76 195 200 205

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79 Ser Ile Arg His Asn Leu Ser Leu His Ser Lys Phe Ile Arg Val Gln
80 210 215 220
83 Asn Glu Gly Thr Gly Lys Ser Ser Trp Trp Met Leu Asn Pro Glu Gly
84 225 230 235 240
87 Gly Lys Ser Gly Lys Ser Pro Arg Arg Arg Ala Ala Ser Met Asp Asn
88 245 250 255
91 Asn Ser Lys Phe Ala Lys Ser Arg Gly Arg Ala Ala Lys Lys Lys Ala
92 260 265 270
95 Ser Leu Gln Ser Gly Gln Glu Gly Pro Gly Asp Ser Pro Gly Ser Gln
96 275 280 285
99 Phe Ser Lys Trp Pro Ala Ser Pro Gly Ser His Ser Asn Asp Asp Phe
100 290 295 300
103 Asp Asn Trp Ser Thr Phe Arg Pro Arg Thr Ser Ser Asn Ala Ser Thr
104 305 310 315 320
107 Ile Ser Gly Arg Leu Ser Pro Ile Met Thr Glu Gln Asp Asp Leu Gly
108 325 330 335
111 Asp Gly Asp Val His Ser Leu Val Tyr Pro Pro Ser Ala Ala Lys Met
112 340 345 350
115 Ala Ser Thr Leu Pro Ser Leu Ser Glu Ile Ser Asn Pro Glu Asn Met
116 355 360 365
119 Glu Asn Leu Leu Asp Asn Leu Asn Leu Leu Ser Ser Pro Thr Ser Leu
120 370 375 380
123 Thr Val Ser Thr Gln Ser Ser Pro Gly Ser Met Met Gln Gln Thr Pro
124 385 390 395 400
127 Cys Tyr Ser Phe Ala Pro Pro Asn Thr Ser Leu Asn Ser Pro Ser Pro
128 405 410 415
131 Asn Tyr Ser Lys Tyr Thr Tyr Gly Gln Ser Ser Met Ser Pro Leu Pro
132 420 425 430
135 Gln Met Pro Met Gln Thr Leu Gln Asp Ser Lys Ser Ser Tyr Gly Gly
136 435 440 445
139 Leu Asn Gln Tyr Asn Cys Ala Pro Gly Leu Leu Lys Glu Leu Leu Thr
140 450 455 460
143 Ser Asp Ser Pro Pro His Asn Asp Ile Met Ser Pro Val Asp Pro Gly
144 465 470 475 480
147 Val Ala Gln Pro Asn Ser Arg Val Leu Gly Gln Asn Val Met Met Gly
148 485 490 495
151 Pro Asn Ser Val Met Pro Ala Tyr Gly Ser Gln Ala Ser His Asn Lys
152 500 505 510
155 Met Met Asn Pro Ser Ser His Thr His Pro Gly His Ala Gln Gln Thr
156 515 520 525
159 Ala Ser Val Asn Gly Arg Thr Leu Pro His Val Val Asn Thr Met Pro
160 530 535 540
163 His Thr Ser Ala Met Asn Arg Leu Thr Pro Val Lys Thr Pro Leu Gln
164 545 550 555 560
167 Val Pro Leu Ser His Pro Met Gln Met Ser Ala Leu Gly Ser Tyr Ser
168 565 570 575
171 Ser Val Ser Ser Cys Asn Gly Tyr Gly Arg Met Gly Val Leu His Gln
172 580 585 590
175 Glu Lys Leu Pro Ser Asp Leu Asp Gly Met Phe Ile Glu Arg Leu Asp

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176	595	600	605	
179	Cys Asp Met Glu Ser Ile Ile Arg Asn Asp Pro Met Asp Gly Asp Thr			
180	610	615	620	
183	Leu Asp Phe Asn Phe Asp Asn Val Leu Pro Asn Gln Ser Phe Pro His			
184	625	630	635	640
187	Ser Val Lys Thr Thr His Ser Trp Val Ser Gly			
188	645	650		
191	<210> SEQ ID NO: 2			
192	<211> LENGTH: 2103			
193	<212> TYPE: DNA			
194	<213> ORGANISM: Mus musculus			
197	<220> FEATURE:			
198	<221> NAME/KEY: CDS			
199	<222> LOCATION: (7)..(1965)			
201	<400> SEQUENCE: 2			
202	gtcacc atg gcc gag gcg ccc cag gtg gag acc gac ccg gac ttc			48
203	Met Ala Glu Ala Pro Gln Val Val Glu Thr Asp Pro Asp Phe			
204	1 5 10			
206	gag ccg atg/gcc cgg cag cgc tcc tgc acc tgg ccg ctg ccc agg ccg			96
207	Glu Pro Leu Pro Arg Gln Arg Ser Cys Thr Trp Pro Leu Pro Arg Pro			
208	15 20 25 30			
210	gag ttt aac cag tcc aac tcg acc acc tcc agt ccg gcg ccg tcg ggc			144
211	Glu Phe Asn Gln Ser Asn Ser Thr Thr Ser Ser Pro Ala Pro Ser Gly			
212	35 40 45			
214	ggc gcg gcc gcc aac ccc gac gcc gcg agc ctg gcc tcg gcg tcc			192
215	Gly Ala Ala Ala Asn Pro Asp Ala Ala Ser Leu Ala Ser Ala Ser			
216	50 55 60			
218	gct gtc agc acc gac ttt atg agc aac ctg agc ctg ctg gag gag agt			240
219	Ala Val Ser Thr Asp Phe Met Ser Asn Leu Ser Leu Leu Glu Glu Ser			
220	65 70 75			
222	gag gac ttc gcg cgg gcg cca ggc tgc gtg gcc gtg gcg gcg gct			288
223	Glu Asp Phe Ala Arg Ala Pro Gly Cys Val Ala Val Ala Ala Ala			
224	80 85 90			
226	gcg gcc agc agg ggc ctg tgc ggg gac ttc cag ggc ccc gag gcg ggc			336
227	Ala Ala Ser Arg Gly Leu Cys Gly Asp Phe Gln Gly Pro Glu Ala Gly			
228	95 100 105 110			
230	tgc gtg cac cca gcg ccc cca cag ccc cca ccg acc ggg ccg ctg tcg			384
231	Cys Val His Pro Ala Pro Pro Gln Pro Pro Pro Thr Gly Pro Leu Ser			
232	115 120 125			
234	cag ccc cca ccc gtg cct ccc tcc gct gcc gcc gcg ggg cca ctc			432
235	Gln Pro Pro Pro Val Pro Pro Ser Ala Ala Ala Ala Gly Pro Leu			
236	130 135 140			
238	gcg gga cag ccg cgc aag acc agc tcg tcg cgc cgc aac gcg tgg ggc			480
239	Ala Gly Gln Pro Arg Lys Thr Ser Ser Ser Arg Arg Asn Ala Trp Gly			
240	145 150 155			
242	aac ctg tcg tac gcc gac ctc atc acc aag gcc atc gag agc tca gcc			528
243	Asn Leu Ser Tyr Ala Asp Leu Ile Thr Lys Ala Ile Glu Ser Ser Ala			
244	160 165 170			
246	gag aag agg ctc acc ctg tcg cag atc tac gag tgg atg gtg aag agc			576

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247	Glu	Lys	Arg	Leu	Thr	Leu	Ser	Gln	Ile	Tyr	Glu	Trp	Met	Val	Lys	Ser		
248	175					180					185					190		
250	gtg	ccc	tac	ttc	aag	gat	aag	ggc	gac	agc	aac	agc	tcg	gcg	ggc	tgg	624	
251	Val	Pro	Tyr	Phe	Lys	Asp	Lys	Gly	Asp	Ser	Asn	Ser	Ser	Ala	Gly	Trp		
252													195	200	205			
254	aag	aat	tca	att	cgc	cac	aat	ctg	tcc	ctt	cac	agc	aag	ttt	att	cga	672	
255	Lys	Asn	Ser	Ile	Arg	His	Asn	Leu	Ser	Leu	Asn	His	Ser	Lys	Phe	Ile	Arg	
256													210	215	220			
258	gtg	cag	aat	gaa	gga	act	gga	aag	agt	tct	tgg	tgg	atg	ctc	aat	cca	720	
259	Val	Gln	Asn	Glu	Gly	Thr	Gly	Lys	Ser	Ser	Trp	Trp	Met	Leu	Asn	Pro		
260													225	230	235			
262	gag	gga	ggc	aag	agc	gga	aaa	tca	ccc	cg	aga	aga	gct	gcg	tcc	atg	768	
263	Glu	Gly	Gly	Lys	Ser	Gly	Lys	Ser	Pro	Arg	Arg	Arg	Ala	Ala	Ser	Met		
264													240	245	250			
266	gac	aac	aac	agt	aaa	ttt	gct	aag	agc	cga	ggg	cg	gct	gct	aag	aaa	816	
267	Asp	Asn	Asn	Ser	Lys	Phe	Ala	Lys	Ser	Arg	Gly	Arg	Ala	Ala	Lys	Lys		
268													255	260	265	270		
270	aaa	gca	tct	ctc	cag	tct	ggg	caa	gag	gg	cct	gga	gac	agc	cct	ggg	864	
271	Lys	Ala	Ser	Leu	Gln	Ser	Gly	Gln	Glu	Gly	Pro	Gly	Asp	Ser	Pro	Gly		
272													275	280	285			
274	tct	cag	ttt	tct	aag	tgg	cct	g	cg	agt	cct	ggg	tcc	cac	agc	aac	912	
275	Ser	Gln	Phe	Ser	Lys	Trp	Pro	Ala	Ser	Pro	Gly	Ser	His	Ser	Asn	Asp		
276													290	295	300			
278	gac	ttt	gat	aac	tgg	agt	aca	ttt	cgt	cct	cga	acc	agc	tca	aat	gct	960	
279	Asp	Phe	Asp	Asn	Trp	Ser	Thr	Phe	Arg	Pro	Arg	Thr	Ser	Ser	Asn	Ala		
280													305	310	315			
282	agt	acc	atc	agt	ggg	aga	ctt	tct	ccc	atc	atg	aca	gag	cag	gat	gac	1008	
283	Ser	Thr	Ile	Ser	Gly	Arg	Leu	Ser	Pro	Ile	Met	Thr	Glu	Gln	Asp	Asp		
284													320	325	330			
286	ctg	gga	gat	ggg	gac	gtg	cat	tcc	ctg	gtg	tat	cca	ccc	tct	gct	gcc	1056	
287	Leu	Gly	Asp	Gly	Asp	Val	His	Ser	Leu	Val	Tyr	Pro	Pro	Ser	Ala	Ala		
288													335	340	345	350		
290	aag	atg	g	cg	tct	acg	ctg	ccc	agt	ctg	tct	gaa	atc	agc	aat	cca	gaa	1104
291	Lys	Met	Ala	Ser	Thr	Leu	Pro	Ser	Leu	Ser	Glu	Ile	Ser	Asn	Pro	Glu		
292													355	360	365			
294	aac	atg	gag	aac	ctt	ctg	gat	aat	ctc	aac	ctt	ctc	tcg	tcc	cca	aca	1152	
295	Asn	Met	Glu	Asn	Leu	Leu	Asp	Asn	Leu	Asn	Leu	Leu	Ser	Ser	Pro	Thr		
296													370	375	380			
298	tct	tta	act	gtg	tcc	acc	cag	tcc	tcg	cct	ggc	agc	atg	atg	cag	cag	1200	
299	Ser	Leu	Thr	Val	Ser	Thr	Gln	Ser	Ser	Pro	Gly	Ser	Met	Met	Gln	Gln		
300													385	390	395			
302	aca	cca	tgc	tat	tcg	ttt	gca	ccg	cca	aac	acc	agt	cta	aat	tca	ccc	1248	
303	Thr	Pro	Cys	Tyr	Ser	Phe	Ala	Pro	Pro	Asn	Thr	Ser	Leu	Asn	Ser	Pro		
304													400	405	410			
306	agt	cca	aac	tac	tca	aag	tac	aca	tac	ggc	caa	tcc	agc	atg	agc	cct	1296	
307	Ser	Pro	Asn	Tyr	Ser	Lys	Tyr	Thr	Tyr	Gly	Gln	Ser	Ser	Met	Ser	Pro		
308													415	420	425	430		
310	ttg	ccc	cag	atg	cct	atg	cag	aca	ctt	cag	gac	agc	aaa	tca	agt	tac	1344	
311	Leu	Pro	Gln	Met	Pro	Met	Gln	Thr	Leu	Gln	Asp	Ser	Lys	Ser	Ser	Tyr		

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312	435	440	445	
314	gga gga ttg aac cag tat aac tgt gcc cca gga ctc ttg aaa gag ttg			1392
315	Gly Gly Leu Asn Gln Tyr Asn Cys Ala Pro Gly Leu Leu Lys Glu Leu			
316	450	455	460	
318	ttg act tct gac tct ccc cac aat gac att atg tca ccg gtt gat			1440
319	Leu Thr Ser Asp Ser Pro Pro His Asn Asp Ile Met Ser Pro Val Asp			
320	465. 470	475		
322	ccc gga gtg gcc caa ccc aac aat cgg gtc ctg ggc caa aat gta atg			1488
323	Pro Gly Val Ala Gln Pro Asn Ser Arg Val Leu Gly Gln Asn Val Met			
324	480	485	490	
326	atg ggc cct aat tcg gtc atg cca gcg tat ggc agc cag gca tct cat			1536
327	Met Gly Pro Asn Ser Val Met Pro Ala Tyr Gly Ser Gln Ala Ser His			
328	495	500	505	510
330	aac aaa atg atg aac ccc agc tcc cac acc cac cct gga cat gca cag			1584
331	Asn Lys Met Met Asn Pro Ser Ser His Thr His Pro Gly His Ala Gln			
332	515	520	525	
334	caa acg gct tcg gtc aac ggc cgt acc ctg ccc cat gtg gtg aac acc			1632
335	Gln Thr Ala Ser Val Asn Gly Arg Thr Leu Pro His Val Val Asn Thr			
336	530	535	540	
338	atg cct cac aca tct gcc atg aac cgc ttg acc ccc gtg aag aca cct			1680
339	Met Pro His Thr Ser Ala Met Asn Arg Leu Thr Pro Val Lys Thr Pro			
340	545	550	555	
342	tta caa gtg cct ctg tcc cac ccc atg cag atg agt gcc ctg ggc agc			1728
343	Leu Gln Val Pro Leu Ser His Pro Met Gln Met Ser Ala Leu Gly Ser			
344	560	565	570	
346	tac tcc tcg gtg agc agc tgc aat ggc tat ggt agg atg ggt gtc ctc			1776
347	Tyr Ser Ser Val Ser Ser Cys Asn Gly Tyr Gly Arg Met Gly Val Leu			
348	575	580	585	590
350	cac cag gag aag ctc cca agt gac ttg gat ggc atg ttt att gag cgc			1824
351	His Gln Glu Lys Leu Pro Ser Asp Leu Asp Gly Met Phe Ile Glu Arg			
352	595	600	605	
354	ttg gac tgt gac atg gag tcc atc att cgg aat gac ccc atg gat gga			1872
355	Leu Asp Cys Asp Met Glu Ser Ile Ile Arg Asn Asp Pro Met Asp Gly			
356	610	615	620	
358	gat acc ttg gat ttt aac ttt gat aat gtg ttg ccc aac caa agc ttc			1920
359	Asp Thr Leu Asp Phe Asn Phe Asp Asn Val Leu Pro Asn Gln Ser Phe			
360	625	630	635	
362	cca cac agt gtc aag act aca aca cac agc tgg gtg tca ggc taa			1965
363	Pro His Ser Val Lys Thr Thr His Ser Trp Val Ser Gly			
364	640	645	650	
366	gagtttagtg agcaggctac attaaaaagt ccttcagatt gtctgacagc aggaactgag			2025
368	gagcagtcca aagatgccct tcaccctcc ttatagttt caagattaaa aaaaaaaaaa			2085
370	aaaaaaaaaaaa aaaaaaaaaa			2103
374	<210> SEQ ID NO: 3			
375	<211> LENGTH: 652			
376	<212> TYPE: PRT			
377	<213> ORGANISM: Mus musculus			
379	<400> SEQUENCE: 3			
381	Met Ala Glu Ala Pro Gln Val Val Glu Thr Asp Pro Asp Phe Glu Pro			

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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:10,11,12,13,14,15

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L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date